

NewSequence.txt  
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Monocotyledonous plants having improved growth characteristics  
and a method for making the same

<130> CD-097-PCT

<150> EP 03076719.8

<151> 2003-06-03

<160> 32

<170> PatentIn version 3.2

<210> 1

<211> 2313

<212> DNA

<213> Oryza sativa

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NewSequence.txt

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 <213> Oryza sativa  
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Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val  
 35 40 45

Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val  
 50 55 60

Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser  
 65 70 75 80

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Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala  
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Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile  
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Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser  
115 120 125

Ile Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp  
130 135 140

Val Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser  
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165 170 175

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180 185 190

Leu Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala  
195 200 205

Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser  
210 215 220

Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys  
225 230 235 240

Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met  
245 250 255

Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu  
260 265 270

Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr  
275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala  
290 295 300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val  
305 310 315 320

Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg

325

NewSequence.txt  
330

335

Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu  
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Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu  
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Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val  
370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala  
385 390 395 400

Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala  
405 410 415

Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val  
420 425 430

Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser  
435 440 445

Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser  
450 455 460

Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn  
465 470 475 480

Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His  
485 490 495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro  
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Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr  
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Glu Gln Ser His Gly Gly Arg  
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&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 3

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NewSequence.txt

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NewSequence.txt

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Leu Ile Ser Lys Gly Lys Ser Ser His Leu Leu Val Phe Ser Glu Asp  
65 70 75 80

Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly Phe  
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Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Val Thr Ile Met Leu  
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Phe Gly Ala Val Gly Thr Ile Ile Ser Cys Thr Ile Ile Ser Leu Gly  
115 120 125

Val Thr Gln Phe Phe Lys Lys Leu Asp Ile Gly Thr Phe Asp Leu Gly  
130 135 140

Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val Cys  
145 150 155 160

Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser Leu  
165 170 175

Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Val Phe  
180 185 190

Asn Ala Ile Gln Ser Phe Asp Leu Thr His Leu Asn His Glu Ala Ala  
195 200 205

Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu Leu Ser Thr Leu  
210 215 220

Leu Gly Ala Ala Thr Gly Leu Ile Ser Ala Tyr Val Ile Lys Lys Leu  
225 230 235 240

Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met Leu  
245 250 255

Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Asp Leu Ser Gly  
260 265 270

NewSequence.txt

Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr Trp  
275 280 285

His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His Thr Phe Ala  
290 295 300

Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu Tyr Val Gly Met  
305 310 315 320

Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp Thr Pro Gly  
325 330 335

Thr Ser Ile Ala Val Ser Ser Ile Leu Met Gly Leu Val Met Val Gly  
340 345 350

Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala Lys  
355 360 365

Lys Asn Gln Ser Glu Lys Ile Asn Phe Asn Met Gln Val Val Ile Trp  
370 375 380

Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Tyr Asn  
385 390 395 400

Lys Phe Thr Arg Ala Gly His Thr Asp Val Arg Gly Asn Ala Ile Met  
405 410 415

Ile Thr Ser Thr Ile Thr Val Cys Leu Phe Ser Thr Val Val Phe Gly  
420 425 430

Met Leu Thr Lys Pro Leu Ile Ser Tyr Leu Leu Pro His Gln Asn Ala  
435 440 445

Thr Thr Ser Met Leu Ser Asp Asp Asn Thr Pro Lys Ser Ile His Ile  
450 455 460

Pro Leu Leu Asp Gln Asp Ser Phe Ile Glu Pro Ser Gly Asn His Asn  
465 470 475 480

Val Pro Arg Pro Asp Ser Ile Arg Gly Phe Leu Thr Arg Pro Thr Arg  
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Thr Val His Tyr Tyr Trp Arg Gln Phe Asp Asp Ser Phe Met Arg Pro  
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NewSequence.txt  
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NewSequence.txt

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 35 40 45  
 Met Asn Glu Ser Ile Thr Ala Leu Leu Ile Gly Ile Cys Thr Gly Val  
 50 55 60  
 Val Ile Leu Leu Phe Ser Gly Gly Lys Ser Ser His Ile Leu Val Phe  
 65 70 75 80  
 Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn  
 85 90 95  
 Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr  
 100 105 110  
 Ile Thr Ser Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Val Ile Ile

115

120

Thr Thr Gly Ala Thr Phe Ala Phe Lys Arg Met Asp Ile Gly Pro Leu  
130 135 140

Glu Ile Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp  
145 150 155 160

Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu  
165 170 175

Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val  
180 185 190

Val Leu Phe Asn Ala Ile Gln Ser Phe Asp Leu Asn Gln Leu Asn Pro  
195 200 205

Ser Ile Ala Leu His Phe Leu Gly Asn Phe Leu Tyr Leu Phe Val Ala  
210 215 220

Ser Thr Leu Leu Gly Val Val Thr Gly Leu Leu Ser Ala Tyr Val Ile  
225 230 235 240

Lys Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu  
245 250 255

Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Thr Tyr  
260 265 270

Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His  
275 280 285

Tyr Thr Trp His Asn Val Thr Gln Ser Ser Arg Ile Thr Thr Lys His  
290 295 300

Ser Phe Ala Thr Leu Ser Phe Val Ala Glu Ile Phe Ile Phe Leu Tyr  
305 310 315 320

Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Ser Asp  
325 330 335

Ser Pro Gly Thr Ser Ile Ala Ala Ser Ser Val Leu Leu Gly Leu Ile  
340 345 350

Leu Leu Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn  
355 360 365

NewSequence.txt

Leu Thr Lys Lys Ser Gln His Gln Lys Ile Ser Phe Arg Gln Gln Val  
370 375 380

Ile Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu  
385 390 395 400

Ala Tyr Asn Gln Phe Thr Met Ser Gly His Thr Gln Leu Arg Ser Asn  
405 410 415

Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val  
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Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro His  
435 440 445

Pro Lys Ile Thr Ser Ser Met Thr Thr Thr Glu Ser Thr Thr Pro Lys  
450 455 460

Ser Phe Ile Val Pro Leu Leu Gly Asp Ser Arg Asp Ser Glu Ala Asp  
465 470 475 480

Leu Glu Gly His Glu Ile His Arg Pro Asn Ser Leu Arg Ala Leu Leu  
485 490 495

Ser Thr Pro Thr His Thr Val His Arg Leu Trp Arg Lys Phe Asp Asp  
500 505 510

Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Val Glu  
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## NewSequence.txt

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NewSequence.txt

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 <213> Suaeda maritima subsp. salsa

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 20 25 30  
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 35 40 45  
 Trp Met Asn Glu Ser Ile Thr Ala Leu Leu Ile Gly Leu Ser Thr Gly  
 50 55 60  
 Ile Ile Ile Leu Leu Ile Ser Gly Gly Lys Ser Ser His Leu Leu Val  
 65 70 75 80  
 Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe  
 85 90 95  
 Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile  
 100 105 110  
 Thr Ile Ile Leu Phe Gly Ala Val Gly Thr Leu Val Ser Phe Ile Ile  
 115 120 125  
 Ile Ser Leu Gly Ser Ile Ala Ile Phe Gln Lys Met Asp Ile Gly Ser  
 130 135 140  
 Leu Glu Leu Gly Asp Leu Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr  
 145 150 155 160  
 Asp Ser val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu  
 165 170 175  
 Leu Tyr Ser Leu Val Phe Gly Glu Gly val val Asn Asp Ala Thr Ser  
 180 185 190  
 Val val Leu Phe Asn Ala Ile Gln Asn Phe Asp Leu Thr His Ile Asp  
 195 200 205  
 His Arg Ile Ala Phe Gln Phe Gly Gly Asn Phe Leu Tyr Leu Phe Phe  
 210 215 220

NewSequence.txt

Ala Ser Thr Leu Leu Gly Ala Val Thr Gly Leu Leu Ser Ala Tyr Val  
225 230 235 240

Ile Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala  
245 250 255

Leu Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe  
260 265 270

Tyr Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser  
275 280 285

His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys  
290 295 300

His Ala Phe Ala Thr Leu Ser Phe Val Ala Glu Ile Phe Ile Phe Leu  
305 310 315 320

Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Arg Phe Val Ser  
325 330 335

Asp Ser Pro Gly Thr Ser Val Ala Val Ser Ser Ile Leu Leu Gly Leu  
340 345 350

His Met Val Gly Arg Ala Ala Phe Val Phe Pro Phe Ala Phe Leu Met  
355 360 365

Asn Leu Ser Lys Lys Ser Asn Ser Glu Lys Val Thr Phe Asn Gln Gln  
370 375 380

Ile Val Ile Trp Trp Ala Gly Leu Met Lys Ser Ala Val Ser Val Ala  
385 390 395 400

Leu Ala Tyr Asn Gln Phe Ser Arg Ser Gly His Thr Gln Leu Arg Gly  
405 410 415

Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr  
420 425 430

Met Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Leu Phe Met Leu Pro  
435 440 445

Gln Pro Lys His Phe Thr Ser Ala Ser Thr Val Ser Asp Leu Gly Ser  
450 455 460

Pro Lys Ser Phe Ser Leu Pro Leu Leu Glu Asp Arg Gln Asp Ser Glu  
465 470 475 480

NewSequence.txt

Ala Asp Leu Gly Asn Asp Asp Glu Glu Ala Tyr Pro Arg Gly Thr Ile  
485 490 495

Ala Arg Pro Thr Ser Leu Arg Met Leu Leu Asn Ala Pro Thr His Thr  
500 505 510

Val His His Tyr Trp Arg Arg Phe Asp Asp Tyr Phe Met Arg Pro Val  
515 520 525

Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr Glu  
530 535 540

Gln Ser Ile Thr Asn Phe Val Thr Glu Asn Ile Ser  
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<211> 1623  
<212> DNA  
<213> Zea mays

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NewSequence.txt

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taa 1623

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<210> 10  
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 <213> Zea mays

<400> 10

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Ser Thr Ser Asp His Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala  
 20 25 30

Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg  
 35 40 45

Trp Val Asn Glu Ser Thr Ala Leu Ile Val Gly Leu Gly Thr Gly Thr  
 50 55 60

Val Ile Leu Met Ile Ser Arg Gly Val Val Ile His Val Leu Val Phe  
 65 70 75 80

Ser Glu Asp Leu Phe Phe Phe Tyr Leu Leu Pro Pro Ile Ile Phe Asn  
 85 90 95

Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr  
 100 105 110

Ile Thr Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Thr Val Ile  
 115 120 125

Ser Leu Gly Ala Leu Gly Leu Ile Ser Arg Leu Asn Ile Gly Ala Leu  
 130 135 140



NewSequence.txt

Glu Leu Gly Asp Tyr Leu Ala Leu Gly Ala Ile Phe Ser Ala Thr Asp  
 145 150 155 160  
 Ser Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Phe Leu  
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 Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val  
 180 185 190  
 Val Val Phe Asn Ala Leu Gln Asn Phe Asp Ile Thr His Ile Asp Ala  
 195 200 205  
 Glu Val Val Phe His Leu Leu Gly Asn Phe Phe Tyr Leu Phe Leu Leu  
 210 215 220  
 Ser Thr Val Leu Gly Val Ala Thr Gly Leu Ile Ser Ala Leu Val Ile  
 225 230 235 240  
 Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu  
 245 250 255  
 Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Ala  
 260 265 270  
 Leu Ser Gly Ile Leu Thr Val Phe Phe Gly Cys Ile Val Met Ser His  
 275 280 285  
 Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His  
 290 295 300  
 Ala Phe Ala Thr Leu Ser Phe Leu Ala Glu Thr Phe Leu Phe Leu Tyr  
 305 310 315 320  
 Val Gly Met Asp Ala Leu Asp Ile Asp Lys Trp Arg Ser Val Ser Asp  
 325 330 335  
 Thr Pro Gly Lys Ser Leu Ala Ile Ser Ser Ile Leu Met Gly Leu Val  
 340 345 350  
 Met Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn  
 355 360 365  
 Leu Ala Lys Lys Thr Glu His Glu Lys Ile Ser Trp Lys Gln Gln Val  
 370 375 380  
 Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu  
 Page 17

385

390

400

Ala Tyr Lys Lys Phe Thr Arg Ala Gly His Thr Gln Val Arg Gly Asn  
405 410 415

Ala Ile Met Ile Thr Ser Thr Ile Ile Val Val Leu Phe Ser Thr Met  
420 425 430

Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His  
435 440 445

Arg Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu  
450 455 460

His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Glu Pro  
465 470 475 480

Thr Asn Ile Pro Arg Pro Ser Ser Ile Arg Gly Glu Phe Leu Thr Met  
485 490 495

Thr Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Ala Phe Met  
500 505 510

Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser  
515 520 525

Pro Thr Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala  
530 535 540

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<211> 1623  
<212> DNA  
<213> Zea mays

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NewSequence.txt

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ccgaagtcac tgcactcacc ttgctgaca tcccagctcg gaagctccat cgaagagccg	1440
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cataggtact ggagaaaatt tgatgacaaa ttcattgcgc caatgtttgg cggcaggggc	1560
ttcgtaccct tcgtccctgg ttcaccaacg gagaggaatc cccacgatct ttcgaagccc	1620
taa	1623

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 <212> PRT  
 <213> Zea mays

<400> 12

Met Gly Leu Gly Val Asp Ala Glu Thr Val Arg Leu Gly Val Leu Ser  
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Ser Thr Ser Asp His Ala Ser Val Val Ser Asn Asn Phe Phe Val Ala  
 20 25 30

Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg  
 35 40 45

Met Val Asn Glu Ser Ile Thr Ala Leu Leu Val Gly Leu Gly Thr Gly  
 50 55 60

Thr Val Ile Leu Met Ile Ser Arg Gly Val Ser Ile His Val Leu Val

## NewSequence.txt

65                      70                      75                      80  
 Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe  
                             85                      90                      95  
 Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile  
                             100                      105                      110  
 Thr Ile Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile  
                             115                      120                      125  
 Ile Ser Leu Gly Ala Met Gly Leu Phe Lys Lys Leu Asp Val Gly Pro  
                             130                      135                      140  
 Leu Glu Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr  
                             145                      150                      155                      160  
 Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu  
                             165                      170                      175  
 Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser  
                             180                      185                      190  
 Ile Val Val Phe Asn Ala Leu Gln Asn Phe Asp Ile Thr His Ile Asn  
                             195                      200                      205  
 Ala Glu Val Val Phe His Leu Leu Gly Asn Phe Leu Tyr Leu Phe Leu  
                             210                      215                      220  
 Leu Ser Thr Val Leu Gly Val Ala Thr Gly Leu Ile Ser Ala Leu Val  
                             225                      230                      235                      240  
 Ile Lys Lys Ile Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala  
                             245                      250                      255  
 Leu Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe  
                             260                      265                      270  
 Ala Leu Ser Gly Ile Leu Thr Val Phe Phe Gly Cys Ile Val Met Ser  
                             275                      280                      285  
 His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys  
                             290                      295                      300  
 His Ala Phe Ala Thr Leu Ser Phe Leu Ala Glu Thr Phe Ile Phe Leu  
                             305                      310                      315                      320

NewSequence.txt

Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Arg Ser Val Ser  
 325 330 335

Asp Thr Pro Gly Lys Ser Ile Ala Ile Ser Ser Ile Leu Met Gly Leu  
 340 345 350

Val Met Leu Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser  
 355 360 365

Asn Leu Ala Lys Lys Asn Glu His Glu Lys Ile Ser Trp Lys Gln Gln  
 370 375 380

Val Val Ile Trp Trp Ser Gly Leu Met Arg Gly Ala Val Ser Met Ala  
 385 390 395 400

Leu Ala Tyr Asn Lys Phe Thr Arg Ala Gly His Thr Glu Val Arg Gly  
 405 410 415

Asn Glu Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr  
 420 425 430

Val Val Phe Gly Leu Leu Thr Lys Pro Leu Ile Arg Leu Leu Met Pro  
 435 440 445

His Arg His Leu Thr Met Leu Ser Asp Asp Ser Thr Pro Lys Ser Leu  
 450 455 460

His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Ser Ile Glu Glu Pro  
 465 470 475 480

Thr Gln Ile Pro Arg Pro Thr Asn Ile Arg Gly Glu Phe Thr Thr Met  
 485 490 495

Thr Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Lys Phe Met  
 500 505 510

Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser  
 515 520 525

Pro Thr Glu Arg Asn Pro His Asp Leu Ser Lys Pro  
 530 535 540

<210> 13  
 <211> 1620  
 <212> DNA  
 <213> Zea mays

<400> 13  
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NewSequence.txt

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 <212> PRT  
 <213> Zea mays  
 <400> 14

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1

5

10

15

NewSequence.txt

Ala Glu His Pro Gln Val Val Pro Asn Ser Val Phe Ile Ala Leu Leu  
20 25 30

Cys Leu Cys Leu Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Val  
35 40 45

Asn Glu Ser Ile Thr Ala Ile Leu Val Gly Ala Ala Thr Gly Thr Val  
50 55 60

Ile Leu Leu Ile Ser Lys Gly Lys Ser Ser His Ile Leu Val Phe Asp  
65 70 75 80

Glu Glu Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala  
85 90 95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Ile Thr Ile  
100 105 110

Ile Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Phe Val Ile Ile Ser  
115 120 125

Leu Gly Ala Met Gly Leu Phe Lys Lys Leu Asp Val Gly Pro Leu Glu  
130 135 140

Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser  
145 150 155 160

Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr  
165 170 175

Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val  
180 185 190

Leu Phe Asn Ala Val Gln Lys Ile Asp Phe Glu His Leu Thr Gly Glu  
195 200 205

Val Ala Leu Gln Val Phe Gly Asn Phe Leu Tyr Leu Phe Ser Thr Ser  
210 215 220

Thr Val Leu Gly Ile Ala Thr Gly Leu Ile Thr Ala Phe Val Leu Lys  
225 230 235 240

Thr Leu Tyr Phe Gly Arg His Ser Thr Thr Arg Glu Leu Ala Ile Met  
245 250 255

Val Leu Met Ala Tyr Leu Ser Phe Met Leu Ala Glu Leu Phe Ser Leu

260

NewSequence.txt  
265

270

Ser Gly Ile Ile Thr Val Phe Phe Cys Gly Val Leu Met Ser His Val  
275 280 285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Ser Arg His Val  
290 295 300

Phe Ala Met Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val  
305 310 315 320

Gly Thr Asp Ala Leu Asp Phe Thr Lys Trp Lys Thr Ser Ser Leu Ser  
325 330 335

Phe Gly Lys Ser Leu Gly Val Ser Ser Val Leu Leu Gly Leu Val Leu  
340 345 350

Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu  
355 360 365

Ser Lys Lys His Pro Gly Glu Lys Ile Thr Ile Arg Gln Gln Val Val  
370 375 380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala  
385 390 395 400

Phe Asn Lys Phe Thr Arg Ala Gly His Thr Gln Val Arg Gly Asn Ala  
405 410 415

Ile Met Ile Thr Ser Thr Ile Ile Val Val Leu Phe Ser Thr Val Val  
420 425 430

Phe Gly Leu Leu Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro His Arg  
435 440 445

Asn Ala Thr Ser Met Leu Ser Asp Asp Ser Ser Pro Lys Ser Leu His  
450 455 460

Ser Pro Leu Leu Thr Ser Gln Leu Ile Ser Ser Ile Glu Glu Pro Thr  
465 470 475 480

Gln Ile Pro Arg Pro Thr Asn Ile Arg Gly Glu Phe Met Thr Met Thr  
485 490 495

Arg Thr Val His Arg Tyr Trp Arg Lys Phe Asp Asp Lys Phe Met Arg  
500 505 510



NewSequence.txt

Pro Met Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro  
515 520 525

Thr Glu Arg Ser Ser Pro Asp Leu Ser Lys Ala  
530 535

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<212> DNA  
<213> Zea mays

<400> 15

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gacctcttct tcattctatct attgccgccc attattttca atgccgggtt ccagggtgaag	300
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accattaccg tgggtctgtt ctctacgatg gtctttggca tgattacaaa gccactgatc	1320
aggctgcttt tgctcgtc tggacatccg agagaattat cggaaccgtc gtcaccaag	1380
agcttcata gtcctcttct tacctcgcaa cagggatctg acctggagtc gacaaccaat	1440
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NewSequence.txt

tactggcgga agttcgatga cgcacttatg agaccgggtgt tcggggggacg tggtttcgtg 1560  
ccatttggtc ccgggcagecc aaccgagcga aatccaccg atctgtccaa agcctga 1617

<210> 16  
<211> 538  
<212> PRT  
<213> Zea mays

<400> 16

Met Gly Tyr Gln Val Val Ala Ala Gln Leu Lys Leu Ala Ser Ser Ala  
1 5 10 15

Asp His Ala Ser Val Val Ile Ile Thr Leu Phe Val Ala Leu Leu Cys  
20 25 30

Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Leu Asn  
35 40 45

Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Gly Thr Gly Val Val Ile  
50 55 60

Leu Leu Ile Ser Arg Gly Lys Asn Ser Arg Leu Leu Val Phe Ser Glu  
65 70 75 80

Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly  
85 90 95

Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile Thr  
100 105 110

Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser Leu  
115 120 125

Gly Ala Ile Ala Thr Phe Ser Arg Met Ser Ile Gly Thr Leu Asp Val  
130 135 140

Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser Val  
145 150 155 160

Cys Thr Leu Gln Val Leu His Gln Asp Glu Thr Pro Phe Leu Tyr Ser  
165 170 175

Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val Leu  
180 185 190

Phe Asn Ala Val Gln Lys Ile Gln Phe Thr His Ile Asn Ala Trp Thr  
195 200 205

NewSequence.txt

Ala Leu Gln Leu Ile Gly Asn Phe Leu Tyr Leu Phe Ser Thr Ser Thr  
 210 215 220

Leu Leu Gly Ile Gly Thr Gly Leu Ile Thr Ala Phe Val Leu Lys Lys  
 225 230 235 240

Leu Tyr Phe Gly Arg His Ser Thr Thr Arg Glu Leu Ala Ile Met Ile  
 245 250 255

Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Ser Leu Ser  
 260 265 270

Gly Leu Leu Thr Val Phe Phe Cys Gly Val Leu Met Ser His Val Thr  
 275 280 285

Trp His Asn Val Thr Glu Ser Ser Arg Thr Thr Ser Arg His Val Phe  
 290 295 300

Ala Thr Leu Ser Phe Ile Ser Glu Thr Phe Ile Phe Leu Tyr Val Gly  
 305 310 315 320

Met Asp Ala Leu Asp Phe Glu Lys Trp Lys Thr Ser Ser Leu Ser Phe  
 325 330 335

Gly Gly Thr Leu Gly Val Ser Gly Val Leu Met Gly Leu Val Met Leu  
 340 345 350

Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Ala  
 355 360 365

Lys Lys His Gln Ser Glu Lys Ile Ser Phe Arg Met Gln Val Val Ile  
 370 375 380

Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu Ala Leu  
 385 390 395 400

Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile  
 405 410 415

Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe  
 420 425 430

Gly Met Ile Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly  
 435 440 445

His Pro Arg Glu Leu Ser Glu Pro Ser Ser Pro Lys Ser Phe His Ser

450

455

NewSequence.txt  
460

Pro Leu Leu Thr Ser Gln Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn  
465 470 475 480

Ile Val Arg Pro Ser Ser Leu Arg Gly Leu Leu Thr Lys Pro Thr His  
485 490 495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro  
500 505 510

Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Thr  
515 520 525

Glu Arg Asn Pro Pro Asp Leu Ser Lys Ala  
530 535

&lt;210&gt; 17

&lt;211&gt; 2564

&lt;212&gt; DNA

&lt;213&gt; Hordeum vulgare

&lt;400&gt; 17

```

aacggaacct tctccagata ccccgcccg cgcgaaaagaa tagaggagaa tcccgacctc      60
cccgcccgcg cggctgcgca tctgcccccc ctctctctcc ctctctcgctc cccaccccg      120
gtttcccggtg ccattctttc cctccccacc ccggcccccg gcacgaagca gcggcggaga      180
cggggccagg aggaggagga gctcgggtgt tcttcgtctc cccgtcgatt cgtctccgga      240
ttagcgccgc cggccgttcc ccgagggctc cgtccgggtt gattcgatct gattgaaaaa      300
gcccgcgtct tccccgagg gcgcgcgctc gctcgccgga gctagctgtg tctcgttcgg      360
ccgggctcaa ggaagaagag taacgggagg gatggcggtt gaagtgggtg cggcgcagtt      420
ggcgcggctg agcgacgcgc tggtcacctc ggaccacgcc tccgtggtct ccatcaacct      480
cttcgtcgcg ctgctctgcg cctgcatcgt cctcgccac ctctctcgagg agaaccgctg      540
gctcaacgag tccatcacgc cctcatcat cgggctgtgc accggcgtgg tgatcctgat      600
gaccaccaag ggaagagct cgcacgtgct cgtcttcagc gaggacctct tcttcataata      660
ctctctccct cccatcatct tcaacgcggg ttccaggtg aagaagaagc agttcttccg      720
gaatttcattg acaatcacat tattcggcgc tgcggggacg atgatttcat tcttcacaat      780
ctctcttgct gccattgcga tattcagcaa gatgaacatt gggacactgg atgtatcaga      840
ttttctcgca attggagcca tctttccgc gacagattct gtctgcactt tacaggttct      900
caatcaggac gagacgcctt ttctgtacag tctagttttc ggggaagggtg ttgtgaacga      960
tgccacatca gtcgtgcttt tcaacgcgct ccagaacttc gatcctaacc aaatcgatgc      1020

```

NewSequence.txt

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ttctactgac cgtgagggtg cgcttatgat gctcatggcc tacctctcat atatgctagc 1200
tgagctgctt gatttgagtg gcatcctcac cgtgttcttc tgtggtattg tgatgtcgca 1260
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cgagaagtgg aaatttgcta gtgacagccc tggcaaatcc atcggaataa gctcaatttt 1440
gctaggatta gttctggttg gaagagctgc ttttgtcttc ccgctttcat tcttatccaa 1500
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```

<210> 18  
 <211> 538  
 <212> PRT  
 <213> Hordeum vulgare  
 <400> 18

Met Ala Phe Glu Val Val Ala Ala Gln Leu Ala Arg Leu Ser Asp Ala  
 1 5 10 15

NewSequence.txt

Leu Ala Thr Ser Asp His Ala Ser Val Val Ser Ile Asn Leu Phe Val  
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 35 40 45  
 Arg Trp Leu Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr  
 50 55 60  
 Gly Val Val Ile Leu Met Thr Thr Lys Gly Lys Ser Ser His Val Leu  
 65 70 75 80  
 Val Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile  
 85 90 95  
 Phe Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe  
 100 105 110  
 Met Thr Ile Thr Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe  
 115 120 125  
 Thr Ile Ser Leu Ala Ala Ile Ala Ile Phe Ser Lys Met Asn Ile Gly  
 130 135 140  
 Thr Leu Asp Val Ser Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala  
 145 150 155 160  
 Thr Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro  
 165 170 175  
 Phe Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr  
 180 185 190  
 Ser Val Val Leu Phe Asn Ala Leu Gln Asn Phe Asp Pro Asn Gln Ile  
 195 200 205  
 Asp Ala Ile Val Ile Leu Lys Phe Leu Gly Asn Phe Cys Tyr Leu Phe  
 210 215 220  
 Val Ser Ser Thr Phe Leu Gly Val Phe Ser Gly Leu Leu Ser Ala Tyr  
 225 230 235 240  
 Ile Ile Lys Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val  
 245 250 255  
 Ala Leu Met Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu  
 260 265 270

NewSequence.txt

Leu Asp Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met  
 275 280 285  
 Ser His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr  
 290 295 300  
 Lys His Ala Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe  
 305 310 315 320  
 Leu Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Ala  
 325 330 335  
 Ser Asp Ser Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly  
 340 345 350  
 Leu Val Leu Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu  
 355 360 365  
 Ser Asn Leu Thr Lys Lys Thr Glu Leu Glu Lys Ile Ser Trp Arg Gln  
 370 375 380  
 Gln Ile Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile  
 385 390 395 400  
 Ala Leu Ala Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His  
 405 410 415  
 Gly Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser  
 420 425 430  
 Thr Met Leu Phe Gly Ile Leu Thr Lys Pro Leu Ile Arg Phe Leu Leu  
 435 440 445  
 Pro Ala Ser Ser Asn Gly Asp Pro Ser Glu Pro Ser Ser Pro Lys Ser  
 450 455 460  
 Leu His Ser Pro Leu Leu Thr Ser Met Leu Gly Ser Asp Met Glu Ala  
 465 470 475 480  
 Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys  
 485 490 495  
 Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu  
 500 505 510  
 Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly

515

520

NewSequence.txt  
525Ser Pro Thr Asp Pro Asn Val Ile Val Ala  
530 535<210> 19  
<211> 2422  
<212> DNA  
<213> Triticum aestivum

<400> 19  
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tcaccgaagt cctgtcactc tctctctc acaagccagc taggctcggg cctggaggcg 1440  
cctctcccca tctgtaggcc ctccagcctc cggatgctca tcaccaagcc gacccacacc 1500



NewSequence.txt

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tttgcttcca gtccaaaaaa aa 2422

```

<210> 20  
 <211> 538  
 <212> PRT  
 <213> Triticum aestivum

<400> 20

Met Gly Tyr Gln Val Val Ala Ala Gln Leu Ala Arg Leu Ser Gly Ala  
 1 5 10 15

Leu Gly Thr Ser Asp His Ala Ser Val Val Ser Ile Thr Leu Phe Val  
 20 25 30

Ala Leu Leu Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn  
 35 40 45

Arg Trp Leu Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr  
 50 55 60

Gly Val Val Ile Leu Met Thr Thr Lys Gly Lys Ser Ser His Val Leu  
 65 70 75 80

Val Phe Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile  
 85 90 95

NewSequence.txt

Phe Asn Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe  
 100 105 110  
 Met Ala Ile Thr Leu Phe Gly Ala Val Gly Thr Met Met Ser Phe Phe  
 115 120 125  
 Thr Ile Ser Leu Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly  
 130 135 140  
 Thr Leu Asp Val Ser Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala  
 145 150 155 160  
 Thr Asp Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro  
 165 170 175  
 Phe Leu Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr  
 180 185 190  
 Ser Val Val Leu Phe Asn Ala Leu Gln Asn Phe Asp Pro Asn Gln Ile  
 195 200 205  
 Asp Ala Ile Val Ile Leu Lys Phe Leu Gly Asn Phe Cys Tyr Leu Phe  
 210 215 220  
 Val Ser Ser Thr Phe Leu Gly Val Phe Thr Gly Leu Leu Ser Ala Tyr  
 225 230 235 240  
 Val Ile Lys Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val  
 245 250 255  
 Ala Leu Val Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu  
 260 265 270  
 Leu Asp Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met  
 275 280 285  
 Ser His Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr  
 290 295 300  
 Lys His Ala Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe  
 305 310 315 320  
 Leu Tyr Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Ala  
 325 330 335  
 Ser Asp Ser Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly  
 340 345 350

NewSequence.txt

Leu Val Leu Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu  
355 360 365

Ser Asn Leu Thr Lys Lys Thr Glu Leu Glu Lys Ile Ser Trp Arg Gln  
370 375 380

Gln Ile Val Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile  
385 390 395 400

Ala Leu Ala Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His  
405 410 415

Gly Asn Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser  
420 425 430

Thr Met Leu Phe Gly Ile Leu Thr Lys Pro Leu Ile Arg Phe Leu Leu  
435 440 445

Pro Ala Ser Ser Asn Gly Ala Ala Ser Asp Pro Ala Ser Pro Lys Ser  
450 455 460

Leu His Ser Pro Leu Leu Thr Ser Gln Leu Gly Ser Asp Leu Glu Ala  
465 470 475 480

Pro Leu Pro Ile Val Arg Pro Ser Ser Leu Arg Met Leu Ile Thr Lys  
485 490 495

Pro Thr His Thr Ile His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu  
500 505 510

Met Arg Pro Met Phe Gly Gly Arg Gly Phe Val Pro Tyr Ser Pro Gly  
515 520 525

Ser Pro Thr Asp Pro Asn Val Leu Val Glu  
530 535

<210> 21  
<211> 1726  
<212> DNA  
<213> Oryza sativa

<400> 21  
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gactacgact cgatcgtcgc gatcaacatc ttcgtggcgc tgctgtgcag ctgcattgtg 180  
atcgggcacc tgctggaagg gaaccgggtg gtcaatgaat ccacaccgc gcttgtcatg 240

NewSequence.txt

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ctggtttttg gtgaaggggt tgtcaatgat gctacatctg ttgtgctctt taatgcaatt 660
gaagacattg atattgctaa ttttgatagc cttgttctac tagcgttcat aggaaatitt 720
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attattaaga aactatgttt tgccagacac tcaactgaca gagaagttgc tatcatgata 840
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ctctatgttg ggatggatgc actggacatt gaaaaatgga aattagctag cagcagtcct 1080
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tcttcaage agcaagtaat catatggttg gcaggtctca tgagaggagc agtatcaata 1260
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cctttcgtgc ctggttcgcc agtggagcgg agcatccatg gatctcaact gggcactgtg 1680
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<210> 22  
 <211> 544  
 <212> PRT  
 <213> Oryza sativa  
 <400> 22

Met Gly Leu Asp Leu Gly Ala Leu Val Leu Lys Ser Gly Gly Leu Leu  
 1 5 10 15

NewSequence.txt

Val Ser Asp Tyr Asp Ser Ile Val Ala Ile Asn Ile Phe Val Ala Leu  
20 25 30

Leu Cys Ser Cys Ile Val Ile Gly His Leu Leu Glu Gly Asn Arg Trp  
35 40 45

Val Asn Glu Ser Ile Thr Ala Leu Val Met Gly Leu Ile Thr Gly Gly  
50 55 60

Val Ile Leu Leu Val Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe  
65 70 75 80

Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn  
85 90 95

Ala Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Arg Asn Phe Met Thr  
100 105 110

Ile Ile Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Val Ile Ile  
115 120 125

Ser Leu Gly Ala Met Thr Leu Phe Lys Lys Leu Asp Val Gly Pro Leu  
130 135 140

Gln Leu Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp  
145 150 155 160

Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu  
165 170 175

Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val  
180 185 190

Val Leu Phe Asn Ala Ile Glu Asp Ile Asp Ile Ala Asn Phe Asp Ser  
195 200 205

Leu Val Leu Leu Ala Phe Ile Gly Asn Phe Leu Tyr Leu Phe Phe Thr  
210 215 220

Ser Thr Leu Leu Gly Val Val Ala Gly Leu Leu Ser Ala Tyr Ile Ile  
225 230 235 240

Lys Lys Leu Cys Phe Ala Arg His Ser Thr Asp Arg Glu Val Ala Ile  
245 250 255

Met Ile Leu Met Ala Tyr Leu Ser Tyr Met Leu Ser Met Leu Leu Asp  
260 265 270

NewSequence.txt

Leu Ser Gly Ile Leu Thr Val Phe Phe Ser Gly Ile Val Met Ser His  
275 280 285

Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Ile Thr Thr Lys His  
290 295 300

Thr Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Leu Phe Leu Tyr  
305 310 315 320

Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Leu Ala Ser Ser  
325 330 335

Ser Pro Lys Lys Pro Ile Ala Leu Ser Ala Thr Ile Leu Gly Leu Val  
340 345 350

Met Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn  
355 360 365

Leu Ser Lys Lys Glu Thr Arg Pro Lys Ile Ser Phe Lys Gln Gln Val  
370 375 380

Ile Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu  
385 390 395 400

Ala Tyr His Lys Phe Thr Ala Ser Gly His Thr Glu Leu Arg Ile Asn  
405 410 415

Ala Ile Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met  
420 425 430

Val Phe Gly Phe Phe Thr Lys Pro Leu Leu Asn Leu Leu Ile Pro Pro  
435 440 445

Arg Pro Asp Ile Ala Ala Asp Leu Ser Ser Gln Ser Ile Ile Asp Pro  
450 455 460

Leu Leu Gly Ser Leu Leu Gly Ser Asp Phe Asp Val Gly Gln Pro Ser  
465 470 475 480

Pro Gln Asn Asn Leu Gln Leu Leu Leu Thr Ile Gln Thr Arg Ser Val  
485 490 495

His Arg Val Trp Arg Lys Phe Asp Asp Arg Phe Met Arg Pro Met Phe  
500 505 510

Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Pro Val Glu Arg  
515 520 525

NewSequence.txt

Ser Ile His Gly Ser Gln Leu Gly Thr val Thr Glu Ala Glu His Ser  
530 535 540

<210> 23  
<211> 1902  
<212> DNA  
<213> Saccharomyces cerevisiae

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gacctattg caggtgatcc tgatgtagac ttaaaccctg ttacagaaga aatgttctcl 180  
tcatgggcat tgttcattat gttgtccta ttgactctg cattgtggtc tagttaactat 240  
ttaactcaga aacgaattag ggcagtgcat gaaactgtgc tttctatttt ttatgggatg 300  
gttattggct tgataataag gatgtcccc gggcattata ttcaagatac gggtactttt 360  
aattcatcct acttttttaa tgttctattg ccgccaatta ttttaaatag tgggtacgag 420  
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tatctagggt tagaactttt tactgaagta gaactagtct ataagccact gctaattatt 1140  
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gacgagtttg atatagaggc tccaagggcg ataaatttat tgaacggtag ttctattcag 1560

NewSequence.txt

acagatttgg gcccatattc tgacaacaat tctccagata tttcaattga ccaattcgcg 1620  
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 ggccitaatg aaactgagaa tactagccct aaccggcaa ggtcttctat ggataagcgt 1740  
 aatttgagag ataaactggg aacaatcttt aattccgact cacaatgggt tcaaaatttt 1800  
 gatgaacagg tattgaagcc agtattcttg gacaacgttt ctccatcttt acaagattcg 1860  
 gctacgcaat cacctgcaga tttctcttcc caaaaccact ag 1902

<210> 24  
 <211> 633  
 <212> PRT  
 <213> Saccharomyces cerevisiae  
 <400> 24

Met Leu Ser Lys Val Leu Leu Asn Ile Ala Phe Lys Val Leu Leu Thr  
 1 5 10 15

Thr Ala Lys Arg Ala Val Asp Pro Asp Asp Asp Asp Glu Leu Leu Pro  
 20 25 30

Ser Pro Asp Leu Pro Gly Ser Asp Asp Pro Ile Ala Gly Asp Pro Asp  
 35 40 45

Val Asp Leu Asn Pro Val Thr Glu Glu Met Phe Ser Ser Trp Ala Leu  
 50 55 60

Phe Ile Met Leu Leu Leu Leu Ile Ser Ala Leu Trp Ser Ser Tyr Tyr  
 65 70 75 80

Leu Thr Gln Lys Arg Ile Arg Ala Val His Glu Thr Val Leu Ser Ile  
 85 90 95

Phe Tyr Gly Met Val Ile Gly Leu Ile Ile Arg Met Ser Pro Gly His  
 100 105 110

Tyr Ile Gln Asp Thr Val Thr Phe Asn Ser Ser Tyr Phe Phe Asn Val  
 115 120 125

Leu Leu Pro Pro Ile Ile Leu Asn Ser Gly Tyr Glu Leu Asn Gln Val  
 130 135 140

Asn Phe Phe Asn Asn Met Leu Ser Ile Leu Ile Phe Ala Ile Pro Gly  
 145 150 155 160

Thr Phe Ile Ser Ala Val Val Ile Gly Ile Ile Leu Tyr Ile Trp Thr  
 165 170 175



NewSequence.txt

Phe Leu Gly Leu Glu Ser Ile Asp Ile Ser Phe Ala Asp Ala Met Ser  
180 185 190

Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val Thr Ile Leu Ser Ile  
195 200 205

Phe Asn Ala Tyr Lys Val Asp Pro Lys Leu Tyr Thr Ile Ile Phe Gly  
210 215 220

Glu Ser Leu Leu Asn Asp Ala Ile Ser Ile Val Met Phe Glu Thr Cys  
225 230 235 240

Gln Lys Phe His Gly Gln Pro Ala Thr Phe Ser Ser Val Phe Glu Gly  
245 250 255

Ala Gly Leu Phe Leu Met Thr Phe Ser Val Ser Leu Leu Ile Gly Val  
260 265 270

Leu Ile Gly Ile Leu Val Ala Leu Leu Leu Lys His Thr His Ile Arg  
275 280 285

Arg Tyr Pro Gln Ile Glu Ser Cys Leu Ile Leu Leu Ile Ala Tyr Glu  
290 295 300

Ser Tyr Phe Phe Ser Asn Gly Cys His Met Ser Gly Ile Val Ser Leu  
305 310 315 320

Leu Phe Cys Gly Ile Thr Leu Lys His Tyr Ala Tyr Tyr Asn Met Ser  
325 330 335

Arg Arg Ser Gln Ile Thr Ile Lys Tyr Ile Phe Gln Leu Leu Ala Arg  
340 345 350

Leu Ser Glu Asn Phe Ile Phe Ile Tyr Leu Gly Leu Glu Leu Phe Thr  
355 360 365

Glu Val Glu Leu Val Tyr Lys Pro Leu Leu Ile Ile Val Ala Ala Ile  
370 375 380

Ser Ile Cys Val Ala Arg Trp Cys Ala Val Phe Pro Leu Ser Gln Phe  
385 390 395 400

Val Asn Trp Ile Tyr Arg Val Lys Thr Ile Arg Ser Met Ser Gly Ile  
405 410 415

Thr Gly Glu Asn Ile Ser Val Pro Asp Glu Ile Pro Tyr Asn Tyr Gln

420

NewSequence.txt  
425

430

Met Met Thr Phe Trp Ala Gly Leu Arg Gly Ala Val Gly Val Ala Leu  
 435 440 445

Ala Leu Gly Ile Gln Gly Glu Tyr Lys Phe Thr Leu Leu Ala Thr Val  
 450 455 460

Leu Val Val Val Val Leu Thr Val Ile Ile Phe Gly Gly Thr Thr Ala  
 465 470 475 480

Gly Met Leu Glu Val Leu Asn Ile Lys Thr Gly Cys Ile Ser Glu Glu  
 485 490 495

Asp Thr Ser Asp Asp Glu Phe Asp Ile Glu Ala Pro Arg Ala Ile Asn  
 500 505 510

Leu Leu Asn Gly Ser Ser Ile Gln Thr Asp Leu Gly Pro Tyr Ser Asp  
 515 520 525

Asn Asn Ser Pro Asp Ile Ser Ile Asp Gln Phe Ala Val Ser Ser Asn  
 530 535 540

Lys Asn Leu Pro Asn Asn Ile Ser Thr Thr Gly Gly Asn Thr Phe Gly  
 545 550 555 560

Gly Leu Asn Glu Thr Glu Asn Thr Ser Pro Asn Pro Ala Arg Ser Ser  
 565 570 575

Met Asp Lys Arg Asn Leu Arg Asp Lys Leu Gly Thr Ile Phe Asn Ser  
 580 585 590

Asp Ser Gln Trp Phe Gln Asn Phe Asp Glu Gln Val Leu Lys Pro Val  
 595 600 605

Phe Leu Asp Asn Val Ser Pro Ser Leu Gln Asp Ser Ala Thr Gln Ser  
 610 615 620

Pro Ala Asp Phe Ser Ser Gln Asn His  
 625 630

&lt;210&gt; 25

&lt;211&gt; 1857

&lt;212&gt; DNA

&lt;213&gt; Magnaporthe grisea

&lt;400&gt; 25

atgactttcg atatcgccgg caacctcctg gagctcacca ggcgcgctgc cgaggaaccc

60

NewSequence.txt

gaacctggag gaatggcagt tggccttgcc ctgcgagtgt ttgccgtcga tggactccag	120
gacctcgta gcttcgatta ccaaattctt ttcaacctcc tccttccacc catcatcctc	180
tcgtccggct acgagttaca tcaggccaac ttcttccggc acatcggaac aattctcacg	240
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actttgtcag ctaccgatcc tgtcaccatc atagccatct tcaactcgta caaggtggac	420
ccgaagctgt ataccatcat ctttggagag gccatcctca atgacgctgt ggccattgtc	480
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ccaatgccgc ctacgggcga cgaagaggca gctggtttgc cagcgggggg gagcaggaca	1680
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accgaggacc caacagccct gttcaggcag ctggacgagg actacatcaa accgaagcta	1800
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<210> 26  
<211> 618

## NewSequence.txt

&lt;212&gt; PRT

&lt;213&gt; Magnaporthe grisea

&lt;400&gt; 26

Met Thr Phe Asp Ile Ala Gly Asn Leu Leu Glu Leu Thr Arg Arg Ala  
 1 5 10 15

Ala Glu Glu Pro Glu Pro Gly Gly Met Ala Val Gly Leu Ala Leu Arg  
 20 25 30

Val Phe Ala Val Asp Gly Leu Gln Asp Leu Val Ser Phe Asp Tyr Gln  
 35 40 45

Ile Phe Phe Asn Leu Leu Leu Pro Pro Ile Ile Leu Ser Ser Gly Tyr  
 50 55 60

Glu Leu His Gln Ala Asn Phe Phe Arg His Ile Gly Thr Ile Leu Thr  
 65 70 75 80

Phe Ala Phe Ala Gly Thr Phe Leu Ser Ala Val Val Ile Gly Val Ile  
 85 90 95

Leu Trp Leu Tyr Thr Arg Val Pro Leu Glu Gly Leu Thr Met Asn Trp  
 100 105 110

Ile Asp Ala Ile Ser Val Gly Ala Thr Leu Ser Ala Thr Asp Pro Val  
 115 120 125

Thr Ile Ile Ala Ile Phe Asn Ser Tyr Lys Val Asp Pro Lys Leu Tyr  
 130 135 140

Thr Ile Ile Phe Gly Glu Ala Ile Leu Asn Asp Ala Val Ala Ile Val  
 145 150 155 160

Ile Phe Glu Ser Ala Gln Lys Ser Ala Arg Gly Leu Thr Lys Gly Ser  
 165 170 175

Ala Ala Gly Ile Ser Thr Phe Phe Trp Gly Phe Trp Ile Phe Leu Arg  
 180 185 190

Asp Phe Phe Gly Ser Leu Phe Ile Gly Ala Leu Leu Gly Ile Leu Thr  
 195 200 205

Ala Leu Met Leu Lys Tyr Thr Tyr Leu Arg Arg Phe Pro Lys Leu Glu  
 210 215 220

Ser Cys Leu Ile Val Leu Ile Ala Tyr Ala Thr Tyr Tyr Phe Ser Gln  
 225 230 235 240

NewSequence.txt

Ala Ile His Met Ser Gly Ile Val Ser Leu Leu Phe Cys Gly Ile Thr  
245 250 255

Leu Lys His Tyr Ala Tyr Phe Asn Met Ser Arg Arg Thr Gln Leu Thr  
260 265 270

Thr Lys Tyr Met Phe Gln Val Leu Ala Gln Leu Ser Glu Asn Phe Ile  
275 280 285

Phe Ile Tyr Leu Gly Val Ser Leu Phe Thr Asp Lys Asp Leu Gln Phe  
290 295 300

Gln Pro Leu Leu Ile Ile Val Thr Val Met Ala Val Cys Ala Ala Arg  
305 310 315 320

Trp Val Ala Val Phe Pro Leu Ser Trp Ala Ile Asn Trp Phe His Lys  
325 330 335

Tyr Arg Ala Glu Arg Arg Gly Ile Lys Asn Val Pro Glu Glu Leu Pro  
340 345 350

Tyr Lys Tyr Gln Gly Met Leu Phe Trp Ala Gly Leu Arg Gly Ala Val  
355 360 365

Gly Val Ala Leu Ala Ala Leu Leu Thr Ala Lys Asp His Arg Ala Phe  
370 375 380

Lys Ala Thr Val Leu Val Val Val Val Leu Thr Val Ile Ile Phe Gly  
385 390 395 400

Gly Thr Thr Val Asn Val Leu Glu Ile Leu Glu Ile Arg Thr Gly Val  
405 410 415

Thr Asp Glu Ile Asp Ser Asp Asp Glu Phe Asp Ile Glu Ala Val Gly  
420 425 430

Gly Tyr Tyr Lys Arg Ser Gly Asn Gly Ile Gly Tyr Ser Pro Ala Gly  
435 440 445

Arg Asn Gly Val Val Pro Leu Asp Thr Arg Pro Gly Arg Arg Arg Asp  
450 455 460

Ser Asn Gly Ala Val Gly Gly Arg Asp Ala Ser Gly Trp Ser Ser Gly  
465 470 475 480

His Arg Ser Pro Leu Ser Ala Ala Arg Pro Gly Ser Leu Val Arg Thr  
Page 45

485

NewSequence.txt  
490

495

Gly Ser Thr Arg Glu Glu Ala Glu Arg Leu Asp Leu Leu Gly Asn Pro  
500 505 510

Gly Gly Ser Thr Asp Ser Asp Asp Phe Gly Ser Asp Ile Asp Thr Ser  
515 520 525

Asp Leu Pro Pro Pro Ala Pro Arg Arg Arg Ser Ser Pro Met Pro Pro  
530 535 540

Thr Gly Asp Glu Glu Ala Ala Gly Leu Pro Ala Gly Gly Ser Arg Thr  
545 550 555 560

Arg Ser Asn Thr Glu Thr Gly Gly Leu Ser Ala Thr Ala Ala Ile Arg  
565 570 575

Gln Leu Phe Ser Thr Glu Asp Pro Thr Ala Leu Phe Arg Gln Leu Asp  
580 585 590

Glu Asp Tyr Ile Lys Pro Lys Leu Leu Leu Asp Gly Gly Ala Gly Arg  
595 600 605

Gly Asn Gly Gly Gly Ala Gly Gly Ser Ser  
610 615

<210> 27  
<211> 654  
<212> DNA  
<213> Oryza sativa

<400> 27  
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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180  
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt 240  
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300  
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360  
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc ttgctaccc 420  
atcatgtata tatgatagcc acaaagttac ttgatgatg atatcaaaga acatttttag 480  
gtgcacctaa cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540  
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600  
aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agta 654

NewSequence.txt

<210> 28  
 <211> 941  
 <212> DNA  
 <213> Zea mays

<400> 28  
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 ataatctata gtactacaat aatatcagtg ttttagagaa tcatataaat gaacagttag 180  
 acatgggtcta aaggacaatt gagtattttg acaacaggac tctacagttt tatcttttta 240  
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 tttattagta catccattta gggtttaggg ttaatgggtt ttatagacta attttttag 360  
 tacatctatt ttattctatt ttagcctcta aattaagaaa actaaaactc ttttttagtt 420  
 tttttattta ataatttaga tataaaatag aataaaataa agtgactaaa aattaaacaa 480  
 atacccttta agaaattaaa aaaactaagg aaacattttt cttgtttcga gtagataatg 540  
 ccagcctggt aaacgccgtc gacgagtcta acggacacca accagcgaac cagcagcgtc 600  
 gcgtcgggcc aagcgaagca gacggcacgg catctctgtc gctgcctctg gacccctctc 660  
 gagagttccg ctccaecgtt ggacttgctc cgctgtcggc atccagaaat tgcgtggcgg 720  
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 acgggggatt cctttccac cgtccttcg ctttcccttc ctgccccgcc gtaataaata 840  
 gacacccctt ccacaccctc tttcccaac ctggtgtgtg tggagcgca cacacacaca 900  
 accagatctc ccccaaatcc acccgtcggc acctccgctt c 941

<210> 29  
 <211> 50  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer: prm3122  
 <400> 29  
 ggggacaagt ttgtacaaa aagcaggctt cacaatgggg atggaggtgg 50

<210> 30  
 <211> 48  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> primer: prm3123  
 <400> 30  
 ggggaccact ttgtacaaga aagctgggtg cactgttcat cttcctcc 48

NewSequence.txt

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<210> 31
<211> 11
<212> PRT
<213> artificial sequence

<220>
<223> amiloride binding site

<400> 31
Asp Val Phe Phe Leu Phe Leu Leu Pro Pro Ile
      5                                10

<210> 32
<211> 10
<212> PRT
<213> artificial sequence

<220>
<221> var
<222> 3 4
<223> amioride binding site

<400> 32
Phe Phe Xaa Xaa Leu Leu Pro Pro Ile Ile
      5                                10

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